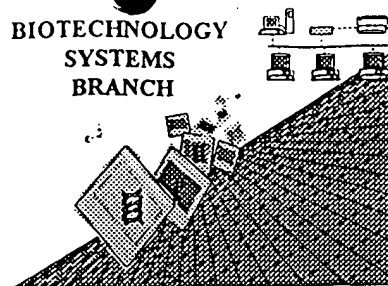


Mr. Pak

1646

BIOTECHNOLOGY
SYSTEMS
BRANCH



#30/SJ
9-13-01

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 08/816,011D

Source: OLPE

Date Processed by STIC: 6/25/2001

RECEIVED

AUG 27 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

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Raw Sequence Listing Error Summary

AUG 27 2001

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ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 08/8/6,0110

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) 65 missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

Re-run

OIPE

RAW SEQUENCE LISTING

DATE: 06/25/2001

PATENT APPLICATION: US/08/816,011D

TIME: 11:28:04

Input Set : A:\11420121.app

Output Set: N:\CRF3\06252001\H816011D.raw

Does Not Comply
Corrected Diskette Needed
P. 6

3 <110> APPLICANT: Pausch, Mark H
 4 Price, Laura A
 6 <120> TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
 7 AND METHODS OF USING SAME
 9 <130> FILE REFERENCE: 01142.0122 SEQUENCE LISTING
 11 <140> CURRENT APPLICATION NUMBER: 08/816,011D
 C--> 12 <141> CURRENT FILING DATE: 2001-06-11
 14 <150> PRIOR APPLICATION NUMBER: 08/332,312
 15 <151> PRIOR FILING DATE: 1994-10-31
 17 <150> PRIOR APPLICATION NUMBER: PCT/US95/14364
 18 <151> PRIOR FILING DATE: 1995-10-25
 20 <160> NUMBER OF SEQ ID NOS: 67
 22 <170> SOFTWARE: PatentIn Ver. 2.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 2441
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Drosophila melanogaster
 29 <400> SEQUENCE: 1
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 31 ctttaaaaga aaaaaaaaaat aataagtcaa aactacaaac cacacagcga aaggcgaaag 120
 32 caacggttcc tgcgagtggt tatttttttt ttcaacaatt tttgatcgta gtgcgacaat 180
 33 ccgtcgagca tgcgcgccga tcgatggatc ctgctgctca tcttctacat atcctacctg 240
 34 atgttcgggg cggaatcta ttaccatatt gagcacggcg aggagaagat atcgcgcgcc 300
 35 gaacagcgca aggcgcaaat tgcaatcaac gaatatctgc tggaggagct gggcgacaag 360
 36 aatacgacca cacaggatga gattcttcaa cggatctcgg attactgtga caaacgggtt 420
 37 acattgccgc cgacatatga tgatacgccc tacacgtgga ccttctacca tgccttcttc 480
 38 ttgcgccttca ccgtttgttc cacggtggga tatgggaata tatcgccaac caccttcgcc 540
 39 ggacggatga tcatgatcgc gtattcgggtg attggcatcc ccgtcaatgg tatcctcttt 600
 40 gccggcctcg gcgaatactt tggacgtacg tttgaagcga tctacagacg ctacaaaaag 660
 41 tacaagatgt ccacggatat gcactatgtc ccgccgcagc tgggattgat caccacgggtg 720
 42 gtgattgccc tgattccggg aatagctctc ttcctgggtc tgccctgcgt ggggtgtcac 780
 43 ctacttcgag aactgggcct atcttccatc tcgctgtact acagctatgt gaccaccaca 840
 44 acaattggat tcggtgacta tgtgccaca tttggagcca accagcccaa ggagtcggc 900
 45 ggctgggtcg tggctatca gatctttgtg atcgtgtggt tcatcttctc gctgggatat 960
 46 cttgtgatga tcatgacatt tatcactcgg ggcctccaga gcaagaagct ggcatacctg 1020
 47 gagcagcagt tgtcctccaa cctgaaggcc acacagaatc gcatctgggtc tggcgctacc 1080
 48 aaggatgtgg gctacctcgg gcgaatgctc aacgagctgt acatcctcaa agtgaagcct 1140
 49 gtgtacaccg atgtagatat cgcctacaca ctgccacgtt ccaattcgtg tccggatctg 1200
 50 agcatgtacc gcgtggagcc ggctcccatt ccagccgga agagggcatt ctccgtgtgc 1260
 51 gccgacatgg ttggcgccca aaggaggcg ggcatggtac acgccaattc cgatacggat 1320
 52 ctaaccaaac tggatcgca gaagacattc gagacggcg aggcgtacca ccagaccacc 1380
 53 gatttgctgg ccaagggtgt caacgcactg gccacggtga agccaccgcc ggcggaacag 1440
 54 gaagatgcgg ctctctatgg tggctatcat ggcttctccg actcccagat cctggccagc 1500
 55 gaatggctgt tctcgacggt caacgagttc acatcaccgc gacgtccaag agcacgtgcc 1560
 56 tgctccgatt tcaatctgga ggcacctcgc tggcagagcg agaggccact gcgttcgagc 1620
 57 cacaacgaat ggacatggag cggcgacaac cagcagatcc aggaggcatt caaccagcgc 1680
 58 tacaagggac agcagcgtgc caacggagca gccaaactcga ccatggtcca tctggagccg 1740

RAW SEQUENCE LISTING

DATE: 06/25/2001

PATENT APPLICATION: US/08/816,011D

TIME: 11:28:04

Input Set : A:\11420121.app

Output Set: N:\CRF3\06252001\H816011D.raw

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60 ccatgccgga tggctcgcga cgtctgtttc ccttcagaa gaagcaccct tcgcaggatc 1860
61 tggagcgcaa gttgtccgtg gtctcggtag ccgagggtgt catctcgcag gaagccagat 1920
62 ccccgtgga ctactacatc aacacgggtc cggcggcctc cagtcaatcc tatttgcgca 1980
63 acggacgcgg tccgccaccg cccttcgaat cgaatggcag cttggccagc ggcggcggcg 2040
64 ggctaacgaa catgggcttc cagatggagg atggagcaac cccgccatcg gcattggcg 2100
65 gtggagccta tcaacgcaag gcgctgctg gcaagcgccg acgcgagagc atctacacc 2160
66 agaatacaag cccatccgct cgccggggca gcatgtatcc gccgaccgcg cagccttgg 2220
67 cccagatgca gatgcgacgc ggcagcttgg caaccagtgg ctctggatcg gcggccatgg 2280
68 cggcagtggc cgcgcgtcgt ggcagcctct tcccagctac agcatcgga tcacgctga 2340
69 cctctgctcc gcgccgaagc agcatattct cggttacctc cgaaggat atgaatgtgc 2400
70 tggagcagac gaccattgcg gatctgattc gtgcgctcga g 2441

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73 <210> SEQ ID NO: 2

74 <211> LENGTH: 618

75 <212> TYPE: PRT

76 <213> ORGANISM: Drosophila melanogaster

78 <400> SEQUENCE: 2

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79 Met Ser Pro Asn Arg Trp Ile Leu Leu Leu Ile Phe Tyr Ile Ser Tyr
80 1 5 10 15
82 Leu Met Phe Gly Ala Ala Ile Tyr Tyr His Ile Glu His Gly Glu Glu
83 20 25 30
85 Lys Ile Ser Arg Ala Glu Gln Arg Lys Ala Gln Ile Ala Ile Asn Glu
86 35 40 45
88 Tyr Leu Leu Glu Glu Leu Gly Asp Lys Asn Thr Thr Thr Gln Asp Glu
89 50 55 60
91 Ile Leu Gln Arg Ile Ser Asp Tyr Cys Asp Lys Pro Val Thr Leu Pro
92 65 70 75 80
94 Pro Thr Tyr Asp Asp Thr Pro Tyr Thr Trp Thr Phe Tyr His Ala Phe
95 85 90 95
97 Phe Phe Ala Phe Thr Val Cys Ser Thr Val Gly Tyr Gly Asn Ile Ser
98 100 105 110
100 Pro Thr Thr Phe Ala Gly Arg Met Ile Met Ile Ala Tyr Ser Val Ile
101 115 120 125
103 Gly Ile Pro Val Asn Gly Ile Leu Phe Ala Gly Leu Gly Glu Tyr Phe
104 130 135 140
106 Gly Arg Thr Phe Glu Ala Ile Tyr Arg Arg Tyr Lys Lys Tyr Lys Met
107 145 150 155 160
109 Ser Thr Asp Met His Tyr Val Pro Pro Gln Leu Gly Leu Ile Thr Thr
110 165 170 175
112 Val Val Ile Ala Leu Ile Pro Gly Ile Ala Leu Phe Leu Val Leu Pro
113 180 185 190
115 Cys Val Gly Val His Leu Leu Arg Glu Leu Gly Leu Ser Ser Ile Ser
116 195 200 205
118 Leu Tyr Tyr Ser Tyr Val Thr Thr Thr Thr Ile Gly Phe Gly Asp Tyr
119 210 215 220
121 Val Pro Thr Phe Gly Ala Asn Gln Pro Lys Glu Phe Gly Gly Trp Phe
122 225 230 235 240
124 Val Val Tyr Gln Ile Phe Val Ile Val Trp Phe Ile Phe Ser Leu Gly
125 245 250 255

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/816,011D

DATE: 06/25/2001

TIME: 11:28:04

Input Set : A:\11420121.app

Output Set: N:\CRF3\06252001\H816011D.raw

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127 Tyr Leu Val Met Ile Met Thr Phe Ile Thr Arg Gly Leu Gln Ser Lys
128           260           265           270
130 Lys Leu Ala Tyr Leu Glu Gln Gln Leu Ser Ser Asn Leu Lys Ala Thr
131           275           280           285
133 Gln Asn Arg Ile Trp Ser Gly Val Thr Lys Asp Val Gly Tyr Leu Arg
134           290           295           300
136 Arg Met Leu Asn Glu Leu Tyr Ile Leu Lys Val Lys Pro Val Tyr Thr
137 305           310           315           320
139 Asp Val Asp Ile Ala Tyr Thr Leu Pro Arg Ser Asn Ser Cys Pro Asp
140           325           330           335
142 Leu Ser Met Tyr Arg Val Glu Pro Ala Pro Ile Pro Ser Arg Lys Arg
143           340           345           350
145 Ala Phe Ser Val Cys Ala Asp Met Val Gly Ala Gln Arg Glu Ala Gly
146           355           360           365
148 Met Val His Ala Asn Ser Asp Thr Asp Leu Thr Lys Leu Asp Arg Glu
149           370           375           380
151 Lys Thr Phe Glu Thr Ala Glu Ala Tyr His Gln Thr Thr Asp Leu Leu
152 385           390           395           400
154 Ala Lys Val Val Asn Ala Leu Ala Thr Val Lys Pro Pro Pro Ala Glu
155           405           410           415
157 Gln Glu Asp Ala Ala Leu Tyr Gly Gly Tyr His Gly Phe Ser Asp Ser
158           420           425           430
160 Gln Ile Leu Ala Ser Glu Trp Ser Phe Ser Thr Val Asn Glu Phe Thr
161           435           440           445
163 Ser Pro Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu
164           450           455           460
166 Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg Ser Ser His Asn Glu
167 465           470           475           480
169 Trp Thr Trp Ser Gly Asp Asn Gln Gln Ile Gln Glu Ala Phe Asn Gln
170           485           490           495
172 Arg Tyr Lys Gly Gln Gln Arg Ala Asn Gly Ala Ala Asn Ser Thr Met
173           500           505           510
175 Val His Leu Glu Pro Asp Ala Leu Glu Glu Gln Leu Arg Asn Asn His
176           515           520           525
178 Arg Val Pro Val Ala Ser Arg Ser Ser Pro Cys Arg Met Val Cys Asp
179           530           535           540
181 Val Cys Phe Pro Ser Arg Arg Ser Thr Pro Arg Arg Ile Trp Ser Ala
182 545           550           555           560
184 Ser Cys Pro Trp Ser Arg Tyr Pro Arg Val Ser Ser Arg Arg Lys Pro
185           565           570           575
187 Asp Pro Arg Trp Thr Thr Thr Ser Thr Arg Ser Arg Arg Pro Pro Val
188           580           585           590
190 Asn Pro Ile Cys Ala Thr Asp Ala Val Arg His Arg Pro Ser Asn Arg
191           595           600           605
193 Met Ala Ala Trp Pro Ala Ala Ala Ala Gly
194           610           615
197 <210> SEQ ID NO: 3
198 <211> LENGTH: 1011
199 <212> TYPE: DNA

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RAW SEQUENCE LISTING

DATE: 06/25/2001

PATENT APPLICATION: US/08/816,011D

TIME: 11:28:04

Input Set : A:\11420121.app

Output Set: N:\CRF3\06252001\H816011D.raw

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200 <213> ORGANISM: Caenorhabditis elegans
202 <400> SEQUENCE: 3
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204 aagaatgcag caacggagac atggacattt tcatcgacca ttttctttgc cgtaaccgtc 120
205 gtcactacca tcggatacgg taatccagtt ccagtgacaa acattggacg gatatggtgt 180
206 atattgttct ccttgcttgg aatacctcta acactggtta ccatcgctga cttggcaggt 240
207 aaattcctat ctgaacatct tgtttggttg tatggaaact attgaaatt aaaatatctc 300
208 atattgtcac gacatcgaaa agaacggaga gagcacgttt gtgagcactg tcacagtcac 360
209 ggaatggggc atgatatgaa tatcgaggag aaaagaattc ctgcattcct ggtattagct 420
210 attctgatag tatatacagc gtttgcggtt gtcctaattg caaaattaga gccgtggtct 480
211 ttcttcactt cattctactg gtccttcatt acaatgacta ctgtcgggtt tggcgacttg 540
212 atgccagaaa gggacggata catgtatatc atattgctct atatcatttt aggtaaaattt 600
213 tcaatgaaaa aaaaacaaaa attcaaaaata tttttaggct ttgcaataac tacaatgtgc 660
214 attgatttgg taggagtaca gtatattcga aagattcatt atttcggaag aaaaattcaa 720
215 gacgctagat ctgcattggc ggtttagga ggaaagtag tccttgatc agaactctac 780
216 gcaaatttaa tgcaaaagcg agctcgtaac atgtcccgag aagcttttat agtggagaat 840
217 ctctatgttt ccaaacacat cataccattc ataccaactg atatccgatg tattcgatat 900
218 attgatcaaa ctgccgatgc tgctaccatt tccacgtcat cgtctgcaat tgatatgcaa 960
219 agttgtagat tttgtcattc aagatattct ctcaatcgtg cattcaataa g 1011
222 <210> SEQ ID NO: 4
223 <211> LENGTH: 336
224 <212> TYPE: PRT
225 <213> ORGANISM: Drosophila melanogaster
227 <400> SEQUENCE: 4
228 Met Ser Asp Gln Leu Phe Val Ala Phe Glu Lys Tyr Phe Leu Thr Ser
229 1 5 10 15
231 Asn Glu Val Lys Lys Asn Ala Ala Thr Glu Thr Trp Thr Phe Ser Ser
232 20 25 30
234 Ser Ile Phe Phe Ala Val Thr Val Val Thr Thr Ile Gly Tyr Gly Asn
235 35 40 45
237 Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser
238 50 55 60
240 Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Asp Leu Ala Gly
241 65 70 75 80
243 Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys
244 85 90 95
246 Leu Lys Tyr Leu Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His
247 100 105 110
249 Val Cys Glu His Cys His Ser His Gly Met Gly His Asp Met Asn Ile
250 115 120 125
252 Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala Ile Leu Ile Val
253 130 135 140
255 Tyr Thr Ala Phe Gly Gly Val Leu Met Ser Lys Leu Glu Pro Trp Ser
256 145 150 155 160
258 Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly
259 165 170 175
261 Phe Gly Asp Leu Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu
262 180 185 190
264 Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Lys Gln Lys Phe

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RAW SEQUENCE LISTING

DATE: 06/25/2001

PATENT APPLICATION: US/08/816,011D

TIME: 11:28:04

Input Set : A:\11420121.app

Output Set: N:\CRF3\06252001\H816011D.raw

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265          195          200          205
267 Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val
268          210          215          220
270 Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln
271 225          230          235          240
273 Asp Ala Arg Ser Ala Leu Ala Val Val Gly Lys Val Val Leu Val
274          245          250          255
276 Ser Glu Leu Tyr Ala Asn Leu Met Gln Lys Arg Ala Arg Asn Met Ser
277          260          265          270
279 Arg Glu Ala Phe Ile Val Glu Asn Leu Tyr Val Ser Lys His Ile Ile
280          275          280          285
282 Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr Ile Asp Gln Thr
283          290          295          300
285 Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ser Ala Ile Asp Met Gln
286 305          310          315          320
288 Ser Cys Arg Phe Cys His Ser Arg Tyr Ser Leu Asn Arg Ala Phe Lys
289          325          330          335
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296 <211> LENGTH: 51
297 <212> TYPE: DNA
298 <213> ORGANISM: Caenorhabditis elegans
300 <400> SEQUENCE: 5
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304 <210> SEQ ID NO: 6
305 <211> LENGTH: 51
306 <212> TYPE: DNA
307 <213> ORGANISM: Caenorhabditis elegans
309 <400> SEQUENCE: 6
310 tcattctact ggctcttcat tacaatgact actgtcgggt ttggcgactt g 51
313 <210> SEQ ID NO: 7
314 <211> LENGTH: 24
315 <212> TYPE: PRT
316 <213> ORGANISM: Drosophila melanogaster
318 <400> SEQUENCE: 7
319 Ala Phe Leu Phe Ser Ile Glu Thr Gln Thr Thr Ile Gly Tyr Gly Phe
320 1 5 10 15
322 Arg Cys Val Thr Asp Glu Cys Pro
323 20
326 <210> SEQ ID NO: 8
327 <211> LENGTH: 24
328 <212> TYPE: PRT
329 <213> ORGANISM: Drosophila melanogaster
331 <400> SEQUENCE: 8
332 Ala Phe Leu Phe Ser Leu Glu Thr Gln Val Thr Ile Gly Tyr Gly Phe
333 1 5 10 15
335 Arg Cys Val Thr Glu Gln Cys Ala
336 20
339 <210> SEQ ID NO: 9
340 <211> LENGTH: 24

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8/6, 0110 6

<210> 65

<211> 4

<212> PRT

<213> Artificial Sequence

see item 11 on Enr summary sheet

<400> 65

Thr Trp Thr Phe

1

FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/08/816,011D

DATE: 06/25/2001

TIME: 11:28:05

Input Set : A:\11420121.app

Output Set: N:\CRF3\06252001\H816011D.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:840 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:1035 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1069 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1070 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:1184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:1189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:1195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:1226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:1346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56
L:1367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56
L:1409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57
L:1430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
L:1463 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60
L:1493 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61
L:1690 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64
L:1699 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1699 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: